

F. Vander Vegt

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P#7

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/323,738

DATE: 07/13/2000
TIME: 15:38:10

Input Set : A:\Uw 3570.app
Output Set: N:\CRF3\07132000\I323738.raw

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3 <110> APPLICANT: Osborne, William R.A.
4      Ramesh, Nagarajan
6 <120> TITLE OF INVENTION: Compositions and Methods for Treating Diabetes
8 <130> FILE REFERENCE: P-UW 3570
10 <140> CURRENT APPLICATION NUMBER: 09/323,738
11 <141> CURRENT FILING DATE: 1999-06-01
13 <150> PRIOR APPLICATION NUMBER: 60/087,660
14 <151> PRIOR FILING DATE: 1998-06-02
16 <150> PRIOR APPLICATION NUMBER: 09/185,852
17 <151> PRIOR FILING DATE: 1998-11-04
19 <160> NUMBER OF SEQ ID NOS: 11
21 <170> SOFTWARE: PatentIn Ver. 2.0
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 450
25 <212> TYPE: DNA
26 <213> ORGANISM: Homo sapiens
28 <220> FEATURE:
29 <221> NAME/KEY: CDS
30 <222> LOCATION: (45)..(377)
32 <400> SEQUENCE: 1
33 gctgcatcag aagaggccat caagcacatc actgtccttc tgcc atg gcc ctg tgg 56
34                                     Met Ala Leu Trp
35                                     1
37 atg cgc ctc ctg ccc ctg ctg gcg ctg ctg gcc ctc tgg gga cct gac 104
38 Met Arg Leu Leu Pro Leu Leu Ala Leu Leu Ala Leu Trp Gly Pro Asp
39      5              10              15              20
41 cca gcc gca gcc ttt gtg aac caa cac ctg tgc ggc tca cac ctg gtg 152
42 Pro Ala Ala Ala Phe Val Asn Gln His Leu Cys Gly Ser His Leu Val
43      25              30              35
45 gaa gct ctc tac cta gtg tgc ggg gaa cga ggc ttc ttc tac aca ccc 200
46 Glu Ala Leu Tyr Leu Val Cys Gly Glu Arg Gly Phe Phe Tyr Thr Pro
47      40              45              50
49 aag acc cgc cgg gag gca gag gac ctg cag gtg ggg cag gtg gag ctg 248
50 Lys Thr Arg Arg Glu Ala Glu Asp Leu Gln Val Gly Gln Val Glu Leu
51      55              60              65
53 ggc ggg ggc cct ggt gca ggc agc ctg cag ccc ttg gcc ctg gag ggg 296
54 Gly Gly Gly Pro Gly Ala Gly Ser Leu Gln Pro Leu Ala Leu Glu Gly
55      70              75              80
57 tcc ctg cag aag cgt ggc att gtg gaa caa tgc tgt acc agc atc tgc 344
58 Ser Leu Gln Lys Arg Gly Ile Val Glu Gln Cys Cys Thr Ser Ile Cys
59      85              90              95              100
61 tcc ctc tac cag ctg gag aac tac tgc aac tag acgcagcccg caggcagccc 397
62 Ser Leu Tyr Gln Leu Glu Asn Tyr Cys Asn
63      105              110
65 cccaccgcgc gcctcctgca ccgagagaga tggaataaag cccttgaacc agc 450
66 <210> SEQ ID NO: 2
69 <211> LENGTH: 110
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70 <212> TYPE: PRT
71 <213> ORGANISM: Homo sapiens
73 <400> SEQUENCE: 2
74 Met Ala Leu Trp Met Arg Leu Leu Pro Leu Leu Ala Leu Leu Ala Leu
75   1           5           10           15
77 Trp Gly Pro Asp Pro Ala Ala Ala Phe Val Asn Gln His Leu Cys Gly
78           20           25           30
80 Ser His Leu Val Glu Ala Leu Tyr Leu Val Cys Gly Glu Arg Gly Phe
81   35           40           45
83 Phe Tyr Thr Pro Lys Thr Arg Arg Glu Ala Glu Asp Leu Gln Val Gly
84   50           55           60
86 Gln Val Glu Leu Gly Gly Gly Pro Gly Ala Gly Ser Leu Gln Pro Leu
87   65           70           75           80
89 Ala Leu Glu Gly Ser Leu Gln Lys Arg Gly Ile Val Glu Gln Cys Cys
90           85           90           95
92 Thr Ser Ile Cys Ser Leu Tyr Gln Leu Glu Asn Tyr Cys Asn
93   100           105           110
96 <210> SEQ ID NO: 3
97 <211> LENGTH: 63
98 <212> TYPE: DNA
99 <213> ORGANISM: Homo sapiens
101 <220> FEATURE:
102 <221> NAME/KEY: CDS
103 <222> LOCATION: (1)..(63)
105 <400> SEQUENCE: 3
106 ggc att gtg gaa caa tgc tgt acc agc atc tgc tcc ctc tac cag ctg   48
107 Gly Ile Val Glu Gln Cys Cys Thr Ser Ile Cys Ser Leu Tyr Gln Leu
108   1           5           10           15
110 gag aac tac tgc aac   63
111 Glu Asn Tyr Cys Asn
112           20
115 <210> SEQ ID NO: 4
116 <211> LENGTH: 21
117 <212> TYPE: PRT
118 <213> ORGANISM: Homo sapiens
120 <400> SEQUENCE: 4
121 Gly Ile Val Glu Gln Cys Cys Thr Ser Ile Cys Ser Leu Tyr Gln Leu
122   1           5           10           15
124 Glu Asn Tyr Cys Asn
125           20
128 <210> SEQ ID NO: 5
129 <211> LENGTH: 90
130 <212> TYPE: DNA
131 <213> ORGANISM: Homo sapiens
133 <220> FEATURE:
134 <221> NAME/KEY: CDS
135 <222> LOCATION: (1)..(90)
137 <400> SEQUENCE: 5
138 ttt gtg aac caa cac ctg tgc ggc tca cac ctg gtg gaa gct ctc tac   48

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139 Phe Val Asn Gln His Leu Cys Gly Ser His Leu Val Glu Ala Leu Tyr
140 1 5 10 15 90
142 cta gtg tgc ggg gaa cga ggc ttc ttc tac aca ccc aag acc
143 Leu Val Cys Gly Glu Arg Gly Phe Phe Tyr Thr Pro Lys Thr
144 20 25 30
147 <210> SEQ ID NO: 6
148 <211> LENGTH: 30
149 <212> TYPE: PRT
150 <213> ORGANISM: Homo sapiens
152 <400> SEQUENCE: 6
153 Phe Val Asn Gln His Leu Cys Gly Ser His Leu Val Glu Ala Leu Tyr
154 1 5 10 15
156 Leu Val Cys Gly Glu Arg Gly Phe Phe Tyr Thr Pro Lys Thr
157 20 25 30
160 <210> SEQ ID NO: 7
161 <211> LENGTH: 4
162 <212> TYPE: PRT
163 <213> ORGANISM: Artificial Sequence
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166 <221> NAME/KEY: SITE
167 <222> LOCATION: (2)
168 <223> OTHER INFORMATION: any amino acid
170 <220> FEATURE:
171 <221> NAME/KEY: SITE
172 <222> LOCATION: (3)
173 <223> OTHER INFORMATION: lysine or arginine or any amino acid (Lys/Arg/Xaa)
175 <220> FEATURE:
176 <223> OTHER INFORMATION: Description of Artificial Sequence: Consensus
177 Sequence
179 <400> SEQUENCE: 7
W--> 180 Arg Xaa Xaa Arg
181 1
184 <210> SEQ ID NO: 8
185 <211> LENGTH: 4
186 <212> TYPE: PRT
187 <213> ORGANISM: Artificial Sequence
189 <220> FEATURE:
190 <221> NAME/KEY: SITE
191 <222> LOCATION: (2)
192 <223> OTHER INFORMATION: any amino acid
194 <220> FEATURE:
195 <221> NAME/KEY: SITE
196 <222> LOCATION: (3)
197 <223> OTHER INFORMATION: Lysine or Arginine (Lys/Arg)
199 <220> FEATURE:
200 <223> OTHER INFORMATION: Description of Artificial Sequence: Consensus
201 Sequence
203 <400> SEQUENCE: 8
W--> 204 Arg Xaa Xaa Arg

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Input Set : A:\Uw 3570.app
 Output Set: N:\CRF3\07132000\I323738.raw

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205 1
208 <210> SEQ ID NO: 9
209 <211> LENGTH: 5
210 <212> TYPE: PRT
211 <213> ORGANISM: Artificial Sequence
213 <220> FEATURE:
214 <223> OTHER INFORMATION: Description of Artificial Sequence: Consensus
215 Sequence
217 <400> SEQUENCE: 9
218 Asp Asp Asp Asp Lys
219 1 5
223 <210> SEQ ID NO: 10
224 <211> LENGTH: 4
225 <212> TYPE: PRT
226 <213> ORGANISM: Artificial Sequence
228 <220> FEATURE:
229 <223> OTHER INFORMATION: Description of Artificial Sequence: Consensus
230 Sequence
232 <400> SEQUENCE: 10
233 Ile Glu Gly Arg
234 1
238 <210> SEQ ID NO: 11
239 <211> LENGTH: 4
240 <212> TYPE: PRT
241 <213> ORGANISM: Artificial Sequence
243 <220> FEATURE:
244 <221> NAME/KEY: SITE
245 <222> LOCATION: (2)
246 <223> OTHER INFORMATION: any amino acid
248 <220> FEATURE:
249 <223> OTHER INFORMATION: Description of Artificial Sequence: Consensus
250 Sequence
252 <400> SEQUENCE: 11
W--> 253 Arg Xaa Lys Arg
254 1

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VERIFICATION SUMMARY
PATENT APPLICATION: US/09/323,738

DATE: 07/13/2000
TIME: 15:38:11

Input Set : A:\Uw 3570.app
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L:180 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:204 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:253 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11